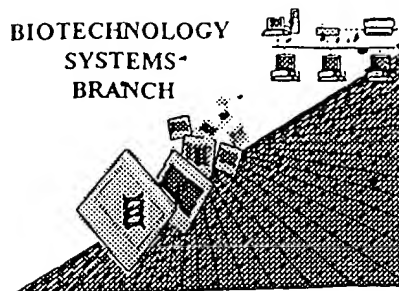


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS-
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/921406
Source: OIPE
Date Processed by STIC: 03/09/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/921406

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/921,406

DATE: 08/09/2001

TIME: 14:36:42

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3 <110> APPLICANT: Yakhini, Zohar

4 Ben-Dor, Amir

5 Sampas, Nick

6 Dougherty, Edward

7 Trent, Jeff

8 Meltzer, Paul

9 Chen, Yidong

10 Weeraratna, Ashani

11 Jiang, Yuan

12 Bittner, Michael

14 <120> TITLE OF INVENTION: Classifying Cancers

16 <130> FILE REFERENCE: 10010313-1

C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/921,406

19 <141> CURRENT FILING DATE: 2001-08-02

21 <160> NUMBER OF SEQ ID NOS: 41

23 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

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27 <212> TYPE: DNA

28 <213> ORGANISM: Homo sapiens

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 E--> 33 ctgttcaagt acactgggaa cagttttaag gtacacctgc agtacantag gagaagcatg 180
 34 agtggataat ctaaaccacag gatcataaca gtgatacgct gcaacacctc tgtgaattcc 240
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Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/921,406

TIME: 14:36:42

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Output Set: N:\CRF3\08092001\I921406.raw

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252 taagcttttag aaatggaatg ccttcaatgg ctcaatctca gaaatggcaa aattctagga 180
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E--> 395 aacaatcaat nagtatttaa tgaattagt tctgtacagt gaaaaataag gtagttgtta 180
E--> 396 aaaaaactta antttttatt ggttttntct acataataaa aaatcagtaa ctatagccac 240
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RAW SEQUENCE LISTING

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PATENT APPLICATION: US/09/921,406

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E--> 490 aggcaggaag ggattctaata acacacacca ggnagcact cctgcccctc agaggccaag 240
E--> 491 gagctgatcc tatattggta tgagggantg ggcttatttt ctgatgacca catgtgggga 300
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541 catcatcatc atcattatta tattaataat attaatacata tccttaaaat ggaaacagta 180
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543 ttaatctttg ctaacaaaaa taatgacaat taattataca gcttcatgta aaatcggctg 300
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RAW SEQUENCE LISTING

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PATENT APPLICATION: US/09/921,406

TIME: 14:36:42

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780 tggagcagac agcttttagc gttcccaatc cttagcaatg ccttagctgg gacgcatagc 4860
781 taatacttta gagaggatga cagatccata aagagagtaa agataagaga aaatgtctaa 4920
782 agcatctgga agggtaaaaa aaaaaatcta tttttgtaca aatgtaattt tatccctcat 4980
783 gtatacttgg atatggcggg gggagggctg ggactgttct gtttctgctt ctagagattg 5040
784 aggtgaaagc ttcgtccgag aaacgccagg acagacgatg gcagaggaga gggctcctgt 5100
785 gacggcgggc aggcttggga ggaaccgcc gcaatggggg tgtcttcctt cggggcagga 5160
786 ggggtggcct gtggttttca aggttttct tcccttctga gtaattttta aagccttgc 5220
787 ctgttgtgtc ctgttgccgg ctctggcctt tctgtgactg actgtgaagt ggcttctccg 5280
788 tacgattgtc tctgaaacat cgtggccgca ggtgcagggt ttgatggaca gtagcattag 5340
789 aattgtggaa aaggaacacg caaagggaga agtgtgagag gagaaacaaa atatgagcgt 5400
790 ttaaaatata tcgccattca g 5421
793 <210> SEQ ID NO: 20
794 <211> LENGTH: 481
795 <212> TYPE: DNA
796 <213> ORGANISM: Homo sapiens
798 <400> SEQUENCE: 20
799 agatgttcac aattcagttt attcaggcaa catattggct gttttcagtg tggacagcta 60
800 cacttaagag caaacatgat gaatctattg agaattcaga ggtagccttt atctgcattt 120
801 ttttttaaac taaaaggatg ttaggaacca cttctgtcga tcgaattatc attaaaagct 180
802 tccatatcag cagtaatgca aggccaataa gaacaattcc agcaaccaca ccagctacaa 240
803 ttggaatgat gtctggacca gtgggacact ctggattctc cacaacatga accatgacct 300
804 cggtgttccc attcactgaa tacgtaaaat agaaccaaca gtccgtcaac atccttctcc 360
805 tttacaatgg gacacaggat caggttggga ccggctgggg gtaatttgtc ccgactttct 420
E--> 806 accttgggta atgttaaaat aggaacattc ctgtgtgcat gtgtccttcc tttcnccntt 480
807 a 481
879 <210> SEQ ID NO: 22
880 <211> LENGTH: 393
881 <212> TYPE: DNA
882 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/921,406

TIME: 14:36:42

Input Set : A:\Agilen11.app

Output Set: N:\CRF3\08092001\I921406.raw

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884 <400> SEQUENCE: 22
E--> 885 tagnannnta ccagggtttta ttatcttttt atcaaaaaaa atcagtaaca gacaacagtg 60
886 tgagaggtgc ctacagagga ggtgctcact ccaacacagc ccaaggggaa gggcactggg 120
E--> 887 ggcagaagag gacccagcca gctgggaccc tgggttgagc tngtgacggg agctaattggc 180
888 cactggtgca gcaagggagg gtggttcccc tcaccgcagc cactgggggc aggaggagac 240
E--> 889 acgacctgcc caggctaagc caccaggmct cccctctcag gagagggagg gtcccagaca 300
E--> 890 acaggcccca gctgggggtct catcagccct ccccattcc ccccnctcc ttaccagggg 360
E--> 891 ggagacaagg gtcgttccag cacagctnag gct 393
946 <210> SEQ ID NO: 24
947 <211> LENGTH: 522
948 <212> TYPE: DNA
949 <213> ORGANISM: Homo sapiens
951 <400> SEQUENCE: 24
952 agcttacaca gtgtttatit gacactgaaa cgaagagctt ctgtacaata gaaagcacag 60
953 tgtgtgcctg gctctaaggc aggatgctaa gagagagaac cagggtcagc tggagaatag 120
954 acaaatgcag agctcagaga ggtgggacat ccagctcgac gaggagatct tgggagaagt 180
955 gaagcaaaga aacttatatg gaagtcatat cggtgagagc gtggtccagc tcctcgctga 240
956 tggctttgta cttcagtttc tgagcgtaca gctcgtcttc taagtcatca atgcttttct 300
957 ccaatttagt tactgacctc tccgcaaaact cagcccgagt ctcagcctcc ttcagcttgt 360
958 cggaaaggac cttgatctct tcctcatatc tgtcttcctt ctgcgagtac ttctcagcct 420
959 gagcctccag tgacttcaaa gttgttcgtc acagttttca attttcttca agctcggcac 480
E--> 960 atttgccttc tgagagtnag ccgntctctt gcacgttcca gg 522
989 <210> SEQ ID NO: 26
990 <211> LENGTH: 397
991 <212> TYPE: DNA
992 <213> ORGANISM: Homo sapiens
994 <400> SEQUENCE: 26
995 gccgtggggg gggaaagtgg gaaggtggag ttttccccag tggcagtget tagcttggat 60
996 cctgagaggg agtaccaggt ggagggttgt ctcaggcacc atcctcctgc cctgggctgc 120
997 tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
E--> 998 gentccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggctctg 240
E--> 999 ctgggttggg gggtcagctc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
E--> 1000 atccatnttn acatagagga ttctgtcagg ctctgggggc aggangcaan gcctttcagt 360
E--> 1001 ntgttctcca aatcttccn caactctnta aaacttt 397
1096 <210> SEQ ID NO: 28
1097 <211> LENGTH: 233
1098 <212> TYPE: DNA
1099 <213> ORGANISM: Homo sapiens
1101 <400> SEQUENCE: 28
E--> 1102 gccatcaatg atcnntgccg gctccccaca cccatggact gcccctccgc catctaccag 60
1103 ctcatgatgc agtgcctggc gcaggagcgt gcccgccgcc ccaagttcgc tgacatcgtc 120
E--> 1104 anatgcctgg acaagctcat tcgtgccctt gactccctca agaccctggc tgactttgac 180
E--> 1105 ccccgctgtg ctatccggct cccagcacg agcggnctcg gagggggtgc cct 233
1182 <210> SEQ ID NO: 30
1183 <211> LENGTH: 503
1184 <212> TYPE: DNA
1185 <213> ORGANISM: Homo sapiens
1187 <400> SEQUENCE: 30
1188 tttttttacg ctaattggca catttgcttt atttatttat ttttaaaaca aactgggttt 60

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RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/921,406

TIME: 14:36:42

Input Set : A:\Agilen11.app

Output Set: N:\CRF3\08092001\I921406.raw

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1189 tttgaattttt ttcttttttg ttcattccat cacattgaaa aggaggaaaa caaaaatgat 120
1190 tttgaattca ctogatatatt tggactcctc agatgaacgg aacattgcac acacacttgg 180
1191 aacagagaga gagagagaga ggaaagtggg ctcccacagg gccacacgca ccagatcaaa 240
1192 taacttggga tacagtgcaa gaatttccca aaatgattga atcatcatta ccaaaaactt 300
E--> 1193 ggccataaca acaccaaggn nacaanaaat gttaaaggcc acactgtttg acttggggat 360
1194 ctttctctgct tttttttttt tttttttaa tgtttgccac acagggggaga aagaggggct 420
E--> 1195 agtgggggtgg ggnaagggca ggtttcacag acgtgagccg gggcagggng gggtttcggg 480
E--> 1196 ttgngctga ggaaggggta ggg 503
1228 <210> SEQ ID NO: 32
1229 <211> LENGTH: 418
1230 <212> TYPE: DNA
1231 <213> ORGANISM: Homo sapiens
1233 <400> SEQUENCE: 32
1234 ttttttttac cgatgcaccc cacagtcagg gtgattttat ttctagaaaa ggtgacaggt 60
1235 gctgcacgtg ggcaggagca ggtcacagtg aggcagggcc aggggcatcc cctctcaac 120
E--> 1236 acaacctagg cgccanagcc taccggccag gtagtagcaa gggctggccc atgtagtgag 180
1237 cccagcatgg ggagacgtg agggcccatg ggcgccaag ccagggggca gcagcctcca 240
1238 aacacgaca gcgccacgtc cctgggggca ggaaaggtg atgcccagg ggcacttctg 300
E--> 1239 ttctctctgc tgggagggcc tgggcaggct tggttttcaa ggacaccagc cgnagggagg 360
E--> 1240 gccttgggca ggttggccag ggnattagga gggcagggga ttgggtttag ncagggga 418
1343 <210> SEQ ID NO: 36
1344 <211> LENGTH: 450
1345 <212> TYPE: DNA
1346 <213> ORGANISM: Homo sapiens
1348 <400> SEQUENCE: 36
1349 tttttttttg tttctaaagt acaaattcag tttattcatc tgtttatgac acagtacaca 60
1350 ggaggcaaag tgtttcacat catagacttc acttccaact ccttggaatg ttcatttctt 120
1351 tggcttacag gagagactag acaggaaggc caggcaatgc ttaggcaact aaaatgaggt 180
1352 tgggggtaat gctaacgtca cctcacagg gatggccacg gggactgtta ttcgcaagct 240
1353 ggttttctag acctgttagc tggaagcatg gtgagcacca tttctgggac gctcaggccg 300
1354 tgtcgggctt cagtcattct caccacacag gtacagcagg cgcttttctg ggtaggtcgc 360
E--> 1355 ccttagtgtc ttgctgggat attaatagta caggggactt gccgtanttt ctcttgatt 420
E--> 1356 tcagacccan ttttcaacat gttccatttc 450
1390 <210> SEQ ID NO: 38
1391 <211> LENGTH: 480
1392 <212> TYPE: DNA
1393 <213> ORGANISM: Homo sapiens
1395 <400> SEQUENCE: 38
1396 tttttttttt tttttttttt tttttaaaca ttagtgttca tagcttccaa gagacatgct 60
1397 gactttcatt tcttgaggta ctctgcacat acgcaccaca tctctatctg gcctttgcat 120
1398 ggagtgaacca tagctccttc tctcttacat tgaatgtaga gaatgtagcc attgtagcag 180
1399 cttgtgttgt cacgcttctt cttttgagca actttcttac actgaagaaa ggcagaatga 240
1400 gtgcttcaga atgtgatttc ctactaacct gttccttggg taggcttttt agtatagtat 300
E--> 1401 tttttttttg ncattttctc catcagcaac caggggagact gcacctgatg gaaaagatat 360
E--> 1402 atgactgctt catgacattc ctaaaactanc tttttttatt ccacatctac gtttttggtg 420
E--> 1403 gagtcccctt tgcattcatt ttttaaggat gatnaaaaaa aaatatcacn aggggggaat 480
1441 <210> SEQ ID NO: 40
1442 <211> LENGTH: 434
1443 <212> TYPE: DNA

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RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/921,406

TIME: 14:36:42

Input Set : A:\Agilen11.app

Output Set: N:\CRF3\08092001\I921406.raw

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1444 <213> ORGANISM: Homo sapiens
1446 <400> SEQUENCE: 40
1447 aagtgaacat taaccattta ttcaaagtta tacaagaatt tgacggatta aagtcttcta 60
1448 tgacataaag ccatttcaaa tagtttcatg tctcagctga gcaggaggag aggggggtgaa 120
E--> 1449 agaataagtg agtagggccc gttggnangc tagacagtaa aaacagactc aacagcagcc 180
1450 gccccccagcc tgctgtcttc cctgattgcc tgcattgtgtt gcattggtag cagcatgctg 240
1451 acggggccaat tttaatgcca ttgacctcat tattaatgtc aaagactcct tcttgaattt 300
E--> 1452 tttcataaat ttcttttgct gtattaataa atgcctcttc tacattngga agcagtctta 360
E--> 1453 gcagacgttt ccatgaagat gagtccatgg tcccgtggca aaaggcttca ncnttccttc 420
E--> 1454 ntttttttac ttct 434

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/921,406

DATE: 08/09/2001

TIME: 14:36:43

Input Set : A:\Agilen11.app

Output Set: N:\CRF3\08092001\I921406.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application Number
L:31 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:204 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:250 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:298 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:394 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
M:340 Repeated in SeqNo=12
L:490 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:539 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
M:340 Repeated in SeqNo=16
L:688 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
M:340 Repeated in SeqNo=18
L:733 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
M:340 Repeated in SeqNo=19
L:806 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:885 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:960 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:998 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
M:340 Repeated in SeqNo=26
L:1102 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:1193 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30
M:340 Repeated in SeqNo=30
L:1236 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
M:340 Repeated in SeqNo=32
L:1355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
M:340 Repeated in SeqNo=36
L:1401 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1449 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40

Volume in drive D:\ is 010802_1245
Directory of D:\

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Appendix A.xls

2869 KB

8/2/01

1 file(s)

Total filesize 2869 KB

2 folder(s)

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